OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/852,472

DATE: 05/24/2001
TIME: 13:17:23

ENTERED

Input Set : A:\97-28C1.SEQ.txt
Output Set: C:\CRF3\05242001\I852472.raw

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 4 <110> APPLICANT: Sheppard, Paul O.
 5        Jelinek, Laura J.
 8 <120> TITLE OF INVENTION: Mammalian Neuro-Growth Factor Like
 9        Protein
11 <130> FILE REFERENCE: 97-28C1
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/852,472
C--> 13 <141> CURRENT FILING DATE: 2001-05-10
13 <150> PRIOR APPLICATION NUMBER: 09/099,295
14 <151> PRIOR FILING DATE: 1998-06-18
16 <150> PRIOR APPLICATION NUMBER: 60/050,143
17 <151> PRIOR FILING DATE: 1997-06-18
19 <160> NUMBER OF SEQ ID NOS: 24
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1297
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (69)...(887)
32 <400> SEQUENCE: 1
33 aagcttggca cgaggtggca cgaggcctcg tgccaagctt ggcacgaggc cgcctggagg   60
34 cacaggcc atg agg ggc tct cag gag gtg ctg ctg atg tgg ctt ctg gtg   110
35            Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val
36             1               5                  10
38 ttg gca gtg ggc ggc aca gag cac gcc tac cgg ccc ggc cgt agg gtg   158
39 Leu Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val
40 15                  20                  25                  30
44 tgt gct gtc cgg gct cac ggg gat cct gtc tcc gag tcg ttc gtg cag   206
45 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln
46                 35                  40                  45
48 cgt gtg tac cag ccc ttc ctc acc acc tgc gac ggg cac cgg gcc tgc   254
49 Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys
50                 50                  55                  60
52 agc acc tac cga acc atc tat agg acc gcc tac cgc cgc agc cct ggg   302
53 Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly
54             65                  70                  75
56 ctg gcc cct gcc agg cct cgc tac gcg tgc tgc ccc ggc tgg aag agg   350
57 Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg
58         80                  85                  90
60 acc agc ggg ctt cct ggg gcc tgt gga gca gca ata tgc cag ccg cca   398
61 Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro
62 95                  100                 105                 110
64 tgc cgg aac gga ggg agc tgt gtc cag cct ggc cgc tgc cgc tgc cct   446
65 Cys Arg Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro
66                 115                 120                 125
68 gca gga tgg cgg ggt gac act tgc cag tca gat gtg gat gaa tgc agt   494
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69 Ala Gly Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser
70           130              135          140
72 gct agg agg ggc ggc tgt ccc cag cgc tgc gtc aac acc gcc ggc agt    542
73 Ala Arg Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser
74        145            150    .            155
76 tac tgg tgc cag tgt tgg gag ggg cac agc ctg tct gca gac ggt aca    590
77 Tyr Trp Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr
78       160              165          170
80 ctc tgt gtg ccc aag gga ggg ccc ccc agg gtg gcc ccc aac ccg aca    638
81 Leu Cys Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr
82 175            180              185              190
86 gga gtg gac agt gca atg aag gaa gaa gtg cag agg ctg cag tcc agg    686
87 Gly Val Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg
88            195              200          205
90 gtg gac ctg ctg gag gag aag ctg cag ctg gtg ctg gcc cca ctg cac    734
91 Val Asp Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His
92        210              215          220
94 agc ctg gcc tcg cag gca ctg gag cat ggg ctc ccg gac ccc ggc agc    782
95 Ser Leu Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser
96        225              230          235
98 ctc ctg gtg cac tcc ttc cag cag ctc ggc cgc atc gac tcc ctg agc    830
99 Leu Leu Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser
100        240              245          250
102 gag cag att tcc ttc ctg gag gag cag ctg ggg tcc tgc tcc tgc aag   878
103 Glu Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
104 255            260              265              270
106 aaa gac tcg tgactgccca gcgccccagg ctggactgag cccctcacgc           927
107 Lys Asp Ser
109 cgccctgcag cccccatgcc cctgcccaac atgctggggg tccagaagcc acctcggggt  987
110 gactgagcgg aaggccaggc agggccttcc tcctcttcct cctcccttc ctcaggaggc 1047
111 tccccagacc ctggcatggg atgggctggg atcttctctg tgaatccacc cctggctacc 1107
112 cccaccctgg ctaccccaac ggcatcccaa ggccaggtgg ccctcagct gagggaaggt 1167
113 acgagctccc tgctggagcc tgggacccat ggcacaggcc aggcagcccg gaggctgggt 1227
114 ggggcctcag tggggctgc tgcctgaccc ccagcacaat aaaaatgaaa cgtgaaaaaa 1287
                                                                    1297
115 aaaaaaaaaa
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 273
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <400> SEQUENCE: 2
123 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
124 1              5              10              15
127 Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
128        20              25              30
129 Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
130        35              40              45
131 Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
132 50              55              60
133 Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
```

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                                              75                    80
134 65                   70
135 Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
136                            85              90                    95
137 Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
138              100                    105              110
139 Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
140        115                    120              125
141 Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
142     130                    135                    140
143 Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
144 145                    150              155                    160
145 Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
146                    165              170                    175
147 Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
148              180              185                    190
149 Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
150        195              200                    205
151 Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
152     210              215                    220
153 Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
154 225              230                    235                    240
155 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln
156              245              250                    255
157 Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
158              260              265              270
159 Ser
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 254
163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 3
167 Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala Val Arg Ala
168 1                5                    10                    15
169 His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val Tyr Gln Pro
170              20                    25                    30
171 Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr Tyr Arg Thr
172        35                    40                    45
173 Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala Pro Ala Arg
174     50                    55                    60
175 Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser Gly Leu Pro
176 65                   70                    75                    80
177 Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly
178                      85              90                    95
179 Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly
180              100                    105              110
181 Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly
182        115                    120              125
183 Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys
184        130                    135              140
```

file://C:\Crf3\Outhold\VsrI852472.htm

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185 Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys
186 145               150                 155                 160
187 Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
188               165                 170                 175
189 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu Glu
190           180                 185                 190
191 Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala Ser Gln
192           195                 200                 205
193 Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu Val His Ser
194     210                 215                 220
195 Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln Ile Ser Phe
196 225                 230                 235                 240
197 Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp Ser
198                 245                 250
200 <210> SEQ ID NO: 4
201 <211> LENGTH: 284
202 <212> TYPE: DNA
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 4
206 ggcggcggcg cgtgcgcgcc ccggatccgg cggccaccca gaggagaagg ccaccccgcc  60
207 tggaggcaca ggccatgagg ggctctcagg aggtgctgct gatgtggctt ctggtgttgg  120
208 cagtgggcgg cacagagcac gcctaccggc ccggccgtag ggtgtgtgct gtccgggctc  180
211 acgggaccc tgtctccgag tcgttcgtgc agcgtgtgta ccagcccttc ctcaccacct  240
212 gcgacgggca ccgggcctgc agcacctacc gaaccatcta tagg                   284
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 40
216 <212> TYPE: DNA
217 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 5                                                    40
220 tgcggcggta ggcggtccta tagatggttc ggtaggtgct
222 <210> SEQ ID NO: 6
223 <211> LENGTH: 18
224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
227 <400> SEQUENCE: 6                                                    18
228 gctgatgtgg cttctggt
230 <210> SEQ ID NO: 7
231 <211> LENGTH: 18
232 <212> TYPE: DNA
233 <213> ORGANISM: Homo sapiens
235 <400> SEQUENCE: 7                                                    18
236 ggtaggcgtg ctctgtgc
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 708
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
243 <400> SEQUENCE: 8
244 Thr His Arg Gly Leu His Ile Ser Ala Leu Ala Thr Tyr Arg Ala Arg
245 1               5                 10                  15
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```
246 Gly Pro Arg Gly Leu Tyr Ala Arg Gly Ala Arg Gly Val Ala Leu Cys
247          20              25              30
250 Tyr Ser Ala Leu Ala Val Ala Leu Ala Arg Gly Ala Leu Ala His Ile
251          35              40              45
252 Ser Gly Leu Tyr Ala Ser Pro Pro Arg Val Ala Leu Ser Glu Arg Gly
253          50              55              60
254 Leu Ser Glu Arg Pro His Glu Val Ala Leu Gly Leu Asn Ala Arg Gly
255 65              70              75              80
256 Val Ala Leu Thr Tyr Arg Gly Leu Asn Pro Arg Pro His Glu Leu Glu
257              85              90              95
258 Thr His Arg Thr His Arg Cys Tyr Ser Ala Ser Pro Gly Leu Tyr His
259          100             105             110
260 Ile Ser Ala Arg Gly Ala Leu Ala Cys Tyr Ser Ser Glu Arg Thr His
261          115             120             125
262 Arg Thr Tyr Arg Ala Arg Gly Thr His Arg Ile Leu Glu Thr Tyr Arg
263          130             135             140
264 Ala Arg Gly Thr His Arg Ala Leu Ala Thr Tyr Arg Ala Arg Gly Ala
265 145             150             155             160
266 Arg Gly Ser Glu Arg Pro Arg Gly Leu Tyr Leu Glu Ala Leu Ala Pro
267              165             170             175
268 Arg Ala Leu Ala Ala Arg Gly Pro Arg Ala Arg Gly Thr Tyr Arg Ala
269              180             185             190
270 Leu Ala Cys Tyr Ser Cys Tyr Ser Pro Arg Gly Leu Tyr Thr Arg Pro
271          195             200             205
272 Leu Tyr Ser Ala Arg Gly Thr His Arg Ser Glu Arg Gly Leu Tyr Leu
273          210             215             220
274 Glu Pro Arg Gly Leu Tyr Ala Leu Ala Cys Tyr Ser Gly Leu Tyr Ala
275 225             230             235             240
276 Leu Ala Ala Leu Ala Ile Leu Glu Cys Tyr Ser Gly Leu Asn Pro Arg
277              245             250             255
278 Pro Arg Cys Tyr Ser Ala Arg Gly Ala Ser Asn Gly Leu Tyr Gly Leu
279          260             265             270
280 Tyr Ser Glu Arg Cys Tyr Ser Val Ala Leu Gly Leu Asn Pro Arg Gly
281          275             280             285
282 Leu Tyr Ala Arg Gly Cys Tyr Ser Ala Arg Gly Cys Tyr Ser Pro Arg
283          290             295             300
284 Ala Leu Ala Gly Leu Tyr Thr Arg Pro Ala Arg Gly Gly Leu Tyr Ala
285 305             310             315             320
286 Ser Pro Thr His Arg Cys Tyr Ser Gly Leu Asn Ser Glu Arg Ala Ser
287              325             330             335
288 Pro Val Ala Leu Ala Ser Pro Gly Leu Cys Tyr Ser Ser Glu Arg Ala
289              340             345             350
292 Leu Ala Ala Arg Gly Ala Arg Gly Gly Leu Tyr Gly Leu Tyr Cys Tyr
293          355             360             365
294 Ser Pro Arg Gly Leu Asn Ala Arg Gly Cys Tyr Ser Val Ala Leu Ala
295 370             375             380
296 Ser Asn Thr His Arg Ala Leu Ala Gly Leu Tyr Ser Glu Arg Thr Tyr
297 385             390             395             400
298 Arg Thr Arg Pro Cys Tyr Ser Gly Leu Asn Cys Tyr Ser Thr Arg Pro
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VERIFICATION SUMMARY   DATE: 05/24/2001
PATENT APPLICATION: US/09/852,472   TIME: 13:17:24

Input Set : A:\97-28C1.SEQ.txt
Output Set: C:\CRF3\05242001\I852472.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date